

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/566,637  
Source: IFWP  
Date Processed by STIC: 2/7/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 02/07/2006

PATENT APPLICATION: US/10/566,637

TIME: 10:20:31

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\02012006\J566637.raw

```

4 <110> APPLICANT: Yukio Goto
5      Hideo Kikkawa
6      Mine Kinoshita
9 <120> TITLE OF INVENTION: METHODS OF TREATMENT WITH LXR AGONISTS
12 <130> FILE REFERENCE: TB00009
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/566,637
C--> 15 <141> CURRENT FILING DATE: 2006-01-27
17 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/008426
W--> 18 <151> PRIOR FILING DATE: 2004-7-27
20 <150> PRIOR APPLICATION NUMBER: 60/490614
W--> 21 <151> PRIOR FILING DATE: 2003-7-28
23 <160> NUMBER OF SEQ ID NOS: 4
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1344
29 <212> TYPE: DNA
30 <213> ORGANISM: human
32 <400> SEQUENCE: 1
33 atgtccttgt ggtctgggggc ccctgtgcct gacattcctc ctgactctgc ggtggagctg 60
34 tggaagccag gcgcacagga tgcaagcagc caggcccagg gaggcagcag ctgcatectc 120
35 agagaggaag ccaggatgcc ccactctgct gggggtactg caggggtggg gctggagggt 180
36 gcagagccca cagccctgct caccagggca gagccccctt cagaaccac agagatccgt 240
37 ccacaaaagc ggaaaaaggg gccagcccc aaaatgctgg ggaacgagct atgcagctg 300
38 tgtggggaca aggcctcggg cttccactac aatgttctga gctgagagg ctgcaaggga 360
39 ttcttccgcc gcagcgtcat caagggagcg cactacatct gccacagtgg cggccactgc 420
40 cccatggaca cctacatgcg tcgcaagtgc caggagtgtc ggcttcgcaa atgccgtcag 480
41 gctggcatgc gggaggagtg tgtcctgtca gaagaacaga tccgcctgaa gaaactgaag 540
42 cggcaagagg aggaacaggc tcatgccaca tccttgcccc ccaggcgttc ctcaccccc 600
43 caaatcctgc ccagctcag cccggaacaa ctgggcatga tcgagaagct cgtcgctgcc 660
44 cagcaacagt gtaaccggcg ctcttttct gaccggcttc gagtacgcc ttggcccatg 720
45 gcaccagatc cccatagccg ggaggcccg cagcagcgt ttgcccactt cactgagctg 780
46 gccatcgtct ctgtgcagga gatagttgac tttgctaaac agctaccggg cttcctgcag 840
47 ctacagccgg aggaccagat tgccctgctg aagacctctg cgatcgagg gatgcttctg 900
48 gagacatctc ggaggtacaa ccctgggagt gagagtatca ccttcctcaa ggatttcagt 960
49 tataaccggg aagactttgc caaagcaggg ctgcaagtgg aattcatcaa ccccatcttc 1020
50 gagttctcca gggccatgaa tgagctgcaa ctcaatgatg ccgagtttgc cttgctcatt 1080
51 gctatcagca tcttctctgc agaccggccc aacgtgcagg accagctcca ggtggagagg 1140
52 ctgcagcaca catatgtgga agccctgcat gcctacgtct ccatccacca tccccatgac 1200
53 cgactgatgt tcccacggat gctaataaaa ctggtgagcc tccggacct gagcagcgtc 1260
54 cactcagagc aagtgtttgc actgcgtctg caggacaaaa agctcccacc gctgctctct 1320
55 gagatctggg atgtgcacga atga                                     1344
57 <210> SEQ ID NO: 2
58 <211> LENGTH: 447

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59 <212> TYPE: PRT
60 <213> ORGANISM: human
62 <400> SEQUENCE: 2
63 Met Ser Leu Trp Leu Gly Ala Pro Val Pro Asp Ile Pro Pro Asp Ser
64 1 5 10 15
65 Ala Val Glu Leu Trp Lys Pro Gly Ala Gln Asp Ala Ser Ser Gln Ala
66 20 25 30
67 Gln Gly Gly Ser Ser Cys Ile Leu Arg Glu Glu Ala Arg Met Pro His
68 35 40 45
69 Ser Ala Gly Gly Thr Ala Gly Val Gly Leu Glu Ala Ala Glu Pro Thr
70 50 55 60
71 Ala Leu Leu Thr Arg Ala Glu Pro Pro Ser Glu Pro Thr Glu Ile Arg
72 65 70 75 80
73 Pro Gln Lys Arg Lys Lys Gly Pro Ala Pro Lys Met Leu Gly Asn Glu
74 85 90 95
75 Leu Cys Ser Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr Asn Val
76 100 105 110
77 Leu Ser Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Ile Lys
78 115 120 125
79 Gly Ala His Tyr Ile Cys His Ser Gly Gly His Cys Pro Met Asp Thr
80 130 135 140
81 Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Arg Lys Cys Arg Gln
82 145 150 155 160
83 Ala Gly Met Arg Glu Glu Cys Val Leu Ser Glu Glu Gln Ile Arg Leu
84 165 170 175
85 Lys Lys Leu Lys Arg Gln Glu Glu Glu Gln Ala His Ala Thr Ser Leu
86 180 185 190
87 Pro Pro Arg Arg Ser Ser Pro Pro Gln Ile Leu Pro Gln Leu Ser Pro
88 195 200 205
89 Glu Gln Leu Gly Met Ile Glu Lys Leu Val Ala Ala Gln Gln Gln Cys
90 210 215 220
91 Asn Arg Arg Ser Phe Ser Asp Arg Leu Arg Val Thr Pro Trp Pro Met
92 225 230 235 240
93 Ala Pro Asp Pro His Ser Arg Glu Ala Arg Gln Gln Arg Phe Ala His
94 245 250 255
95 Phe Thr Glu Leu Ala Ile Val Ser Val Gln Glu Ile Val Asp Phe Ala
96 260 265 270
97 Lys Gln Leu Pro Gly Phe Leu Gln Leu Ser Arg Glu Asp Gln Ile Ala
98 275 280 285
99 Leu Leu Lys Thr Ser Ala Ile Glu Val Met Leu Leu Glu Thr Ser Arg
100 290 295 300
101 Arg Tyr Asn Pro Gly Ser Glu Ser Ile Thr Phe Leu Lys Asp Phe Ser
102 305 310 315 320
103 Tyr Asn Arg Glu Asp Phe Ala Lys Ala Gly Leu Gln Val Glu Phe Ile
104 325 330 335
105 Asn Pro Ile Phe Glu Phe Ser Arg Ala Met Asn Glu Leu Gln Leu Asn
106 340 345 350
107 Asp Ala Glu Phe Ala Leu Leu Ile Ala Ile Ser Ile Phe Ser Ala Asp
108 355 360 365

```

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```

109 Arg Pro Asn Val Gln Asp Gln Leu Gln Val Glu Arg Leu Gln His Thr
110      370                      375                      380
111 Tyr Val Glu Ala Leu His Ala Tyr Val Ser Ile His His Pro His Asp
112 385                      390                      395                      400
113 Arg Leu Met Phe Pro Arg Met Leu Met Lys Leu Val Ser Leu Arg Thr
114                      405                      410                      415
115 Leu Ser Ser Val His Ser Glu Gln Val Phe Ala Leu Arg Leu Gln Asp
116                      420                      425                      430
117 Lys Lys Leu Pro Pro Leu Leu Ser Glu Ile Trp Asp Val His Glu
118      435                      440                      445
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 1383
123 <212> TYPE: DNA
124 <213> ORGANISM: human
126 <400> SEQUENCE: 3
127 atgtcctctc ctaccacgag ttccctggat acccccctgc ctggaaatgg cccccctcag 60
128 cctggcgccc cttcttcttc acccactgta aaggaggagg gtccggagcc gtggccccgg 120
129 ggtccggacc ctgatgtccc aggcactgat gaggccagct cagcctgcag cacagactgg 180
130 gtcaccccag atcccgaaga ggaaccagag cgcaagcgaa agaagggccc agccccgaag 240
131 atgctgggccc acgagctttg ccgtgtctgt ggggacaagg cctccggctt ccactacaac 300
132 gtgctcagct gcgaaggctg caagggcttc ttccggcgca gtgtggtccg tgggtggggccc 360
133 aggcgctatg cctgcccgggg tggcggaacc tgccagatgg acgctttcat gcggcgcaag 420
134 tgccagcagt gccggctgcg caagtgcgaag gaggcagggg tgaggggagca gtgcgtcctt 480
135 tctgaagaac agatccggaa gaagaagatt cggaaacagc agcaggagtc acagtccacag 540
136 tcgcagtcac ctgtggggccc gcagggcagc agcagctcag cctctggggc tggggcttcc 600
137 cctggtggat ctgaggcagg cagccagggc tccggggaag gcgaggggtg ccagctaaca 660
138 gcggctcaag aactaatgat ccagcagttg gtggcgggccc aactgcagtg caacaaacgc 720
139 tccttctccg accagcccaa agtcacgccc tggcccctgg gcgcagaccc ccagtcccga 780
140 gatccccgcc agcaacgctt tgcccacttc acggagctgg ccatcatctc agtccaggag 840
141 atcgctggact tcgctaagca agtgcctggg ttcttgacgc tggggccggga ggaccagatc 900
142 gccctcctga aggcattccac tatcgagatc atgctgctag agacagccag gcgctacaac 960
143 cacgagacag agtgtatcac cttcttgaag gacttcacct acagcaagga cgacttccac 1020
144 cgtgcaggcc tgcaggtgga gttcatcaac cccatcttcg agttctcgcg ggccatgcgg 1080
145 cggtggggccc tggacgacgc tgagtacgcc ctgctcatcg ccatcaacat cttctcgggc 1140
146 gaccggccca acgtgcagga gccggggccgc gtggaggcgt tgcagcagcc ctacgtggag 1200
147 gcgctgctgt cctacacgcg catcaagagg ccgcaggacc agctgcgctt cccgcgcatg 1260
148 ctcatgaagc tggtagcctt gcgcacgctg agctctgtgc actcggagca ggtcttcgcc 1320
149 ttgcggctcc aggacaagaa gctgccgcct ctgctgtcgg agatctggga cgtccacgag 1380
150 tga
152 <210> SEQ ID NO: 4
153 <211> LENGTH: 460
154 <212> TYPE: PRT
155 <213> ORGANISM: human
157 <400> SEQUENCE: 4
158 Met Ser Ser Pro Thr Thr Ser Ser Leu Asp Thr Pro Leu Pro Gly Asn
159 1                      5                      10                      15
160 Gly Pro Pro Gln Pro Gly Ala Pro Ser Ser Pro Thr Val Lys Glu
161      20                      25                      30
162 Glu Gly Pro Glu Pro Trp Pro Gly Gly Pro Asp Pro Asp Val Pro Gly

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```

163          35          40          45
164 Thr Asp Glu Ala Ser Ser Ala Cys Ser Thr Asp Trp Val Ile Pro Asp
165          50          55          60
166 Pro Glu Glu Glu Pro Glu Arg Lys Arg Lys Lys Gly Pro Ala Pro Lys
167 65          70          75          80
168 Met Leu Gly His Glu Leu Cys Arg Val Cys Gly Asp Lys Ala Ser Gly
169          85          90          95
170 Phe His Tyr Asn Val Leu Ser Cys Glu Gly Cys Lys Gly Phe Phe Arg
171          100          105          110
172 Arg Ser Val Val Arg Gly Gly Ala Arg Arg Tyr Ala Cys Arg Gly Gly
173          115          120          125
174 Gly Thr Cys Gln Met Asp Ala Phe Met Arg Arg Lys Cys Gln Gln Cys
175          130          135          140
176 Arg Leu Arg Lys Cys Lys Glu Ala Gly Met Arg Glu Gln Cys Val Leu
177 145          150          155          160
178 Ser Glu Glu Gln Ile Arg Lys Lys Lys Ile Arg Lys Gln Gln Gln Glu
179          165          170          175
180 Ser Gln Ser Gln Ser Gln Ser Pro Val Gly Pro Gln Gly Ser Ser Ser
181          180          185          190
182 Ser Ala Ser Gly Pro Gly Ala Ser Pro Gly Gly Ser Glu Ala Gly Ser
183          195          200          205
184 Gln Gly Ser Gly Glu Gly Glu Gly Val Gln Leu Thr Ala Ala Gln Glu
185          210          215          220
186 Leu Met Ile Gln Gln Leu Val Ala Ala Gln Leu Gln Cys Asn Lys Arg
187 225          230          235          240
188 Ser Phe Ser Asp Gln Pro Lys Val Thr Pro Trp Pro Leu Gly Ala Asp
189          245          250          255
190 Pro Gln Ser Arg Asp Ala Arg Gln Gln Arg Phe Ala His Phe Thr Glu
191          260          265          270
192 Leu Ala Ile Ile Ser Val Gln Glu Ile Val Asp Phe Ala Lys Gln Val
193          275          280          285
194 Pro Gly Phe Leu Gln Leu Gly Arg Glu Asp Gln Ile Ala Leu Leu Lys
195          290          295          300
196 Ala Ser Thr Ile Glu Ile Met Leu Leu Glu Thr Ala Arg Arg Tyr Asn
197 305          310          315          320
198 His Glu Thr Glu Cys Ile Thr Phe Leu Lys Asp Phe Thr Tyr Ser Lys
199          325          330          335
200 Asp Asp Phe His Arg Ala Gly Leu Gln Val Glu Phe Ile Asn Pro Ile
201          340          345          350
202 Phe Glu Phe Ser Arg Ala Met Arg Arg Leu Gly Leu Asp Asp Ala Glu
203          355          360          365
204 Tyr Ala Leu Leu Ile Ala Ile Asn Ile Phe Ser Ala Asp Arg Pro Asn
205          370          375          380
206 Val Gln Glu Pro Gly Arg Val Glu Ala Leu Gln Gln Pro Tyr Val Glu
207 385          390          395          400
208 Ala Leu Leu Ser Tyr Thr Arg Ile Lys Arg Pro Gln Asp Gln Leu Arg
209          405          410          415
210 Phe Pro Arg Met Leu Met Lys Leu Val Ser Leu Arg Thr Leu Ser Ser
211          420          425          430

```

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212	Val	His	Ser	Glu	Gln	Val	Phe	Ala	Leu	Arg	Leu	Gln	Asp	Lys	Lys	Leu
213			435					440					445			
214	Pro	Pro	Leu	Leu	Ser	Glu	Ile	Trp	Asp	Val	His	Glu				
215		450					455					460				

## VERIFICATION SUMMARY

DATE: 02/07/2006

PATENT APPLICATION: US/10/566,637

TIME: 10:20:32

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\02012006\J566637.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:18 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:21 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD